

1009.

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#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/905,243

DATE: 12/03/2001
TIME: 11:52:03

Input Set : N:\Crf3\RULE60\09905243.txt
Output Set: N:\CRF3\12032001\I905243.raw

4 <110> APPLICANT: Taylor, Alexander H
6 <120> TITLE OF INVENTION: Monoclonal Antibodies with Reduced
7 Immunogenicity
9 <130> FILE REFERENCE: P50770
11 <140> CURRENT APPLICATION NUMBER: 09/905,243
12 <141> CURRENT FILING DATE: 2001-07-16
14 <150> PRIOR APPLICATION NUMBER: 09/300,970
15 <151> PRIOR FILING DATE: 1999-04-28
17 <160> NUMBER OF SEQ ID NOS: 97
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 429
23 <212> TYPE: DNA
24 <213> ORGANISM: Pan troglodytes
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)...(429)
30 <400> SEQUENCE: 1
31 atg aaa cac ctg tgg ttc ttc ctc ctg ctg gca gct ccc aga tgg 48
32 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
33 1 5 10 15
35 gtc ctg tcc cag gtt cag ttg cag gag tcg ggc cca gga ctg gtt aag 96
36 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
37 20 25 30
39 cct tca cag acc ttg tcc ctg acc tgc gct gtt tct ggt ggc tcc atc 144
40 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile
41 35 40 45
43 act agt gct tac tac tat tgg agc tgg atc cgc cag tca cca ggg aag 192
44 Thr Ser Ala Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys
45 50 55 60
47 gga ctg gag tgg att ggg agt atc tat tat agt ggg acc att ttc tcc 240
48 Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser
49 65 70 75 80
51 aac cca tcc ctc aag agt cga gtc gcc atg tca gta ggc acg tcc aag 288
52 Asn Pro Ser Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys
53 85 90 95
55 acc cag ttc tcc ctg agc ttg agt tct gtt acc gcc ggc gac acg gcc 336
56 Thr Gln Phe Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
57 100 105 110
59 gtt tac tac tgt gtc aga ggt ctg ctc ctc acc att gga ctg acc aac 384
60 Val Tyr Tyr Cys Ala Arg Gly Leu Leu Leu Thr Ile Gly Leu Thr Asn
61 115 120 125
63 tac tac ttt gac tac tgg ggc ccg gga acc ctg gtc acc gtc ttc 429
64 Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Phe
65 130 135 140
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 414

ENTERED

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Input Set : N:\Crf3\RULE60\09905243.txt
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70 <212> TYPE: DNA
71 <213> ORGANISM: Pan troglodytes
73 <220> FEATURE:
74 <221> NAME/KEY: CDS
75 <222> LOCATION: (1)...(414)
77 <400> SEQUENCE: 2

78 atg aaa cac ctg tgg ttc ttc ctc ctg ctg gca gct ccc aga tgg	48
79 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
80 1 5 10 15	
82 gtc ctg tcc cag gtg cag cta cag gag tgg ggc cca gga cta gtg aag	96
83 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
84 20 25 30	
86 ccg tca cag acc ctg tcc ctc acc tgc ggt gtc tct ggt gcc tcc atc	144
87 Pro Ser Gln Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile	
88 35 40 45	
90 aat agt ggt gtt cat tac tgg gcc tgg ata cgc cag cct gca gga aag	192
91 Asn Ser Gly Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys	
92 50 55 60	
94 gga ctg gag tgg att ggc aat atc tat cat agt ggg agc gcc tac tac	240
95 Gly Leu Glu Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr	
96 65 70 75 80	
98 act cca tcc ctc gag agt cga gtc tcc atg tca ata gag acg tcc aag	288
99 Thr Pro Ser Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys	
100 85 90 95	
102 agc cag ttc ttc cta aac tta aat tct ctg acc gcc gcg gac acg gct	336
103 Ser Gln Phe Phe Leu Asn Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala	
104 100 105 110	
106 atc tat tat tgt gcg aga cga cat act tgc tca gac tac ttt gac ttt	384
107 Ile Tyr Tyr Cys Ala Arg Arg His Thr Ser Ser Asp Tyr Phe Asp Phe	
108 115 120 125	
110 tgg ggc cgc gga atc ctg gtc atc gtc tcc	414
111 Trp Gly Arg Gly Ile Leu Val Ile Val Ser	
112 130 135	
115 <210> SEQ ID NO: 3	
116 <211> LENGTH: 427	
117 <212> TYPE: DNA	
118 <213> ORGANISM: Pan troglodytes	
120 <220> FEATURE:	
121 <221> NAME/KEY: CDS	
122 <222> LOCATION: (1)...(427)	
124 <400> SEQUENCE: 3	
125 atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc gaa gga	48
126 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Glu Gly	
127 1 5 10 15	
129 gtc cgt gca gac gtg cag ctg gtg cag tcc gga gca gag gtg aaa aag	96
130 Val Arg Ala Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
131 20 25 30	
133 ccc ggg gag tct ctg aag atc tcc tgt aag gtc tct gga aat gaa ttt	144
134 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe	

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Input Set : N:\Crf3\RULE60\09905243.txt
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135	35	40	45	
137	acc aac tac tgg atc gcc tgg gtg cgc cag atg tcc ggg aaa ggc ctg			192
138	Thr Asn Tyr Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu			
139	50	55	60	
141	gag tgg atg ggg agc atc tat cct ggt gac tct gat acc aga tac aac			240
142	Glu Trp Met Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn			
143	65	70	75	80
145	ccg tcc ttc caa ggc caa gtc acc ttt tca gcc gac aag tcc atc acc			288
146	Pro Ser Phe Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr			
147	85	90	95	
149	acc gcc tat ttg cag tgg agt agt ctg gag gcc tcg gac acc gcc atg			336
150	Thr Ala Tyr Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met			
151	100	105	110	
153	tac tac tgt gcg agc cga aat cac ttt gtt ttc ggg gaa gtt att act			384
154	Tyr Tyr Cys Ala Ser Arg Asn His Phe Val Phe Gly Glu Val Ile Thr			
155	115	120	125	
157	act ttg acg gct ggg gcc agg gaa acc ctg ggt cac cgt ctc c			427
158	Thr Leu Thr Ala Gly Ala Arg Glu Thr Leu Gly His Arg Leu			
159	130	135	140	
162	<210> SEQ ID NO: 4			
163	<211> LENGTH: 402			
164	<212> TYPE: DNA			
165	<213> ORGANISM: Pan troglodytes			
167	<220> FEATURE:			
168	<221> NAME/KEY: CDS			
169	<222> LOCATION: (1)...(402)			
171	<400> SEQUENCE: 4			
172	ttg ggg ctc cgc tgg gtt ttc ctt gtt gct ttt tta gaa ggt gtc cag			48
173	Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly Val Gln			
174	1	5	10	15
176	tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg			96
177	Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly			
178	20	25	30	
180	ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc agt agg			144
181	Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg			
182	35	40	45	
184	agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg ggg tgg			192
185	Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp			
186	50	55	60	
188	ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg gac tca			240
189	Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser Asp Ser			
190	65	70	75	80
192	gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat tca ctc			288
193	Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu			
194	85	90	95	
196	tat ctg caa atg aac agc ctg aga gcc gac gac gct ttt tat tac			336
197	Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe Tyr Tyr			
198	100	105	110	
200	tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc cag gga			384

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Input Set : N:\Crf3\RULE60\09905243.txt
Output Set: N:\CRF3\12032001\I905243.raw

201 Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly Gln Gly
202 115 120 125 402
204 acc ctg gtc acc gtc tcc
205 Thr Leu Val Thr Val Ser
206 130
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 408
211 <212> TYPE: DNA
212 <213> ORGANISM: Pan troglodytes
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (1)...(408)
218 <400> SEQUENCE: 5
219 atg gaa ttg ggg ctc cgc tgg gtt ttc ctt gtt gct ttt tta gaa ggt 48
220 Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly
221 1 5 10 15
223 gtc cag tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag 96
224 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln
225 20 25 30
227 cct ggg ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc 144
228 Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
229 35 40 45
231 agt agg agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 192
232 Ser Arg Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
233 50 55 60
235 gag tgg ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg 240
236 Glu Trp Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser
237 65 70 75 80
239 gac tca gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat 288
240 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
241 85 90 95
243 tca ctc tat ctg caa atg aac agc ctg aga gcc gac acg gct ttt 336
244 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe
245 100 105 110
247 tat tac tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc 384
248 Tyr Tyr Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly
249 115 120 125
251 cag gga acc ctg gtc acc gtc tcc 408
252 Gln Gly Thr Leu Val Thr Val Ser
253 130 135
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 421
258 <212> TYPE: DNA
259 <213> ORGANISM: Pan troglodytes
261 <220> FEATURE:
262 <221> NAME/KEY: CDS
263 <222> LOCATION: (1)...(421)
265 <400> SEQUENCE: 6
266 atg atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa 48

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Input Set : N:\Crf3\RULE60\09905243.txt
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267	Met Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln		
268	1 5 10 15		
270	gga gtc tgt gca gag gtg cag ctg gtg cag tct gga gca gag gtg aaa	96	
271	Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys		
272	20 25 30		
274	aag ccc ggg gag tct ctg aag atc tcc tgt aag ggc tct gga tac agt	144	
275	Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser		
276	35 40 45		
278	ttt acc aac tac tgg atg ggc tgg tgc cag atg ccc ggg aaa ggc	192	
279	Phe Thr Asn Tyr Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly		
280	50 55 60		
282	ccg gag tgc atg ggg atc atc tat cct gat gac tct gat acc aga tac	240	
283	Pro Glu Cys Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr		
284	65 70 75 80		
286	agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc	288	
287	Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile		
288	85 90 95		
290	agc acc gcc tac cta caa tgg agc aac ctg aag gcc tgc gac acc gcc	336	
291	Ser Thr Ala Tyr Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala		
292	100 105 110		
294	ata tat tac tgt gcg aga tgt tat ggt tgg act act tgc gaa gct ttt	384	
295	Ile Tyr Tyr Cys Ala Arg Cys Tyr Gly Trp Thr Thr Cys Glu Ala Phe		
296	115 120 125		
298	gat atc tgg ggc caa ggg aca atg gtc acc gtc tct t	421	
299	Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser		
300	130 135 140		
303	<210> SEQ ID NO: 7		
304	<211> LENGTH: 417		
305	<212> TYPE: DNA		
306	<213> ORGANISM: Pan troglodytes		
308	<220> FEATURE:		
309	<221> NAME/KEY: CDS		
310	<222> LOCATION: (1)...(417)		
312	<400> SEQUENCE: 7		
313	ttg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc	48	
314	Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser		
315	1 5 10 15		
317	cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag	96	
318	Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln		
319	20 25 30		
321	acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt	144	
322	Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly		
323	35 40 45		
325	agt tac tac tgg agt tgg atc cgg cag ccc gcc ggg aag cga ctg gag	192	
326	Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu		
327	50 55 60		
329	tgg att ggg tat att tat tat agt ggg agt acc tac tac aac cca tcc	240	
330	Trp Ile Gly Tyr Ile Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser		
331	65 70 75 80		

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/905,243

DATE: 12/03/2001

TIME: 11:52:04

Input Set : N:\Crf3\RULE60\09905243.txt

Output Set: N:\CRF3\12032001\I905243.raw